REMARKS

Favorable reconsideration and allowance of the present application are respectfully requested in view of the foregoing amendments and the following remarks.

Claim 4 has been canceled without prejudice or disclaimer. Claims 1-3 and 5 have been amended to more clearly point out the invention or to correct grammatical errors. Accordingly, claims 1-3 and 5 are currently pending and are believed now in the condition of allowance.

Correction of the Form PTO-1449 is acknowledged.

The specification has been amended to comply with 37 CFR §§ 1.821 et seq. Corrected Figs. 6a-6b incorporating the appropriate sequence identifiers are submitted herewith. The sequence entry for *M. terrae* has been deleted. Approval of the corrections and entry of the corrected drawings are requested.

The specification stands objected to because of trademarks which were not capitalized: DYNAZYME®, GENECLEAN®, and BIODYNE® have been amended.

As noted above, the claims have been amended to correct misspellings and grammatical errors. Withdrawal of the claim objections is requested.

Claim Rejection under 35 U.S.C. § 112

Claims 2-5 stand rejected under 35 U.S.C. §112, first paragraph because they are allegedly not enabled for methods employing any "DNA fragment from microorganism to identify." The Examiner, however, recognizes that claims 2-5 are enabled for methods of identifying the species and/or subspecies of a mycobacterial strain in which the DNA fragment to be tested corresponds to the rpoB gene.

Claim 2 has been amended to recite specific restriction enzymes that may be used in the digestion of DNA fragments to obtain DNA fragment length polymorphism patterns in steps a) and d) as well as to limit the sources of DNA fragment to be identified. Claim 2 has been further amended to specifically recite that the rpoB region of the DNA fragment is amplified using specific primers.

Claims 2-5 stand rejected under *35* U.S.C. § 112, second paragraph, as being allegedly indefinite. The claims have been clarified as shown above.

All the changes are made for clarification and support for the changes may be found in the application as originally filed. Withdrawal of the Section 112 rejections is requested.

Claim Rejection under 35 U.S.C. § 102

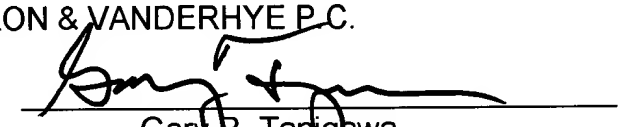
Claims 2-5 stand rejected under 35 U.S.C. § 102(a) as being anticipated by Lee et al. This rejection is overcome by establishing a priority date before the publication of Lee et al. Attached is a certified translation of priority document 1999-46795 (Republic of Korea) filed October 27, 1999.

Withdrawal of the Section 102 rejection is requested.

In light of the above amendments and remarks, Applicants respectfully submit that pending claims 1-3 and 5 as currently presented are now in condition for allowance. Early notice of such action is earnestly solicited and will be greatly appreciated. If any outstanding issues remain, the Examiner is invited to contact the undersigned at the telephone number provided.

Respectfully submitted,

NIXON & VANDERHYE P.C.

By: 

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APPENDIX
MARKED-UP VERSION TO SHOW CHANGES

IN THE SPECIFICATION

The specification is amended as follows.

Paragraph spanning pages 12-13:

PCR amplification. The primer set used to amplify the region of the *rpoB* were 5'-TCAAGGAGAAGCGCTACGA-3' (RPO5', SEQ ID NO:25) and 5'-GGATGTTGATCA GGGTCTGC-3' (RPO3', SEQ ID NO:26) resulting in about 360-bp PCR product (base number 902 to 1261 and codon number 302 to 420 based on the sequence numbers for the *rpoB* gene of *M. tuberculosis*, [GenBank accession No. p47766]). The primer sequences were selected from the region of the *rpoB* genes that have been previously identified from *M. tuberculosis, M. leprae,* and *M. smegmatis* (12, 13, 22). The primers were made to amplify the region between the variable region and conserved region based on the genetic information for the *rpoB* gene of *Escherichia coli.* As a result, PCR products included 171-bp of variable region and 189-bp of conserved region. Variable region was amplified in this experiment based on an assumption that the polymorphic nature of this region might help the clear distinction of each mycobacterial species using molecular biological techniques such as PRA and PCR-DNA hybridization. On the other hand, the region of the *rpoB* gene was also chosen to be flanked by highly conserved sequences, thus can be suitable for PCR amplification of the *rpoB* region of all mycobacterial species using the same set of PCR primers.

First full paragraph at page 13:

PCR was carried out in a final volume of 50 µl with 10 µl of DNA supernatant containing approximately 10 ng of genomic DNA, 10 pmole of each primers, 2 mM $MgCl_2$, 200 μM of deoxynucleotide triphosphates, and 1 unit of ~~DyNAzyme™II~~ DYNAZYME® II DNA polymerase (FINNZYMES, Espoo, Finland). DNA samples were first denatured completely by incubation at 94°C for 5 min before amplification cycle,

then amplified using a cycle that includes (1) denaturation at 94°C for 1 min, (2) primer annealing at 58°C for 1 min, and (3) elongation at 72°C for 1 min for 35 times using a ~~Thermocycler~~ thermocycler (model 9600, Perkin Elmer). After the last amplification cycle, the samples were incubated further at 72°C for 7 min for complete elongation of the final PCR products. Positive and negative controls were always included in each PCR reaction. The positive control was the PCR mix with DNA of reference strain, *M. bovis,* and the negative control was the PCR mix without any DNA. After the PCR, the amplification results were visualized using 1.5% agarose gel electrophoresis and ethidium bromide staining.

Paragraph spanning pages 14-15:

Cloning and sequence analysis. For sequence analysis, PCR products were purified by using a ~~Geneclean~~ GENECLEAN® kit (BIO101, Vista, Calif. USA) from an agarose gel and cloned into TOPO-TA cloning vector (Invitrogen Co., Carlsbad, CA) by the method recommended by the manufacturer. DNA sequencing was done by the dideoxy nucleotide-chain termination method (21) using ARL automatic sequence (Pharmacia Biotechs, Uppsala, Sweden). For each clone, M13 reverse primer and T7 promoter primer were used separately to read sequences from both directions. Sequences were aligned using a multiple sequence alignment program (6).

Table 2 spanning pages 15-16:

Table 2. Oligonucleotide probes designed in this study to develop PCR-probe hybridization assay for Mycobacterial species identification.

Name of oligonucleotides	Sequences of oligonucleotides	Ttarget Mycobacteria
PAN-MYC	GACGTCGTCGCCACCATCGA (nucleotides 108 to 127 of SEQ ID NO:1)	All mycobacterial species
TB	CATGTCGGCGAGCCC (nucleotides 66 to 80 of SEQ ID NO:5)	*M. tuberculosis* complex

Name of oligonucleotides	Sequences of oligonucleotides	Target Mycobacteria
AVIUM	CGGTGAGCCGATCACCA (nucleotides 71 to 87 of SEQ ID NO:15)	*M. avium*
INTRA	CCTGCACGCGGGCGA (nucleotides 62 to 76 of SEQ ID NO:20)	*M. intracellularae*
GORDONAE	GTCGGCGATCCGATCA (nucleotides 69 to 84 of SEQ ID NO:1)	*M. gordonae*
SZULGAI	TCTGAACGTCGGCGAG (nucleotides 61 to 76 of SEQ ID NO:12)	*M. szulgai*
KANSASII	GGCCACGATGACCGTG (nucleotides 155 to 170 of SEQ ID NO:8)	*M. kansasii*
GASTRI	TCTGAACGTCGGCGAG (nucleotides 61 to 76 of SEQ ID NO:12)	*M. gastri*
FORTUITUM	CCTGAACGCCGGCCAG (nucleotides 62 to 77 of SEQ ID NO:19)	*M. fortuitum*
~~FORTUITUM-COM~~	~~GTTCCGGTCGAGGTGG~~	*M. fortuitum complex*
SCROFULACEUM	CGTACGGATGGCCAGC (nucleotides 153 to 168 of SEQ ID NO:9)	*M. scrofulaceum*
CHELONAE	TGGTGACTGCCACCACG (nucleotides 85 to 101 of SEQ ID NO:7)	*M. chelonae*
ABSCESSUS	AGGTGACCACCACCACC (nucleotides 85 to 101 of SEQ ID NO:21)	*M. abscesus*
~~TERRAE~~	~~GCTCAGGACGGTCAGT~~	*M. terrae*
ULCERANS/ MARINUM	GGCCAGCCCATCACC (nucleotides 72 to 86 of SEQ ID NO:10)	*M. ulcerans / M. marinum*
~~GENAVANSE/SIMIAE~~	~~CCAGCCACGATGACG~~	*M. genavanse / M. simiae*

Paragraph spanning pages 16-17:

PCR-reverse blot hybridization. All oligonucleotide probes to be applied on the membrane were synthesized with 5' terminal amino group, which link the oligonucleotides to the ~~Biodyne~~ BIODYNE® C membrane (Pall BioSupport, East Hills, NY) by forming covalent bond with negatively charged carboxyl group fixed on the

membrane. Before blotting the oligonucleotide probes, the ~~Biodyne~~ BIODYNE® C membrane was activated by incubating in 10 ml of freshly prepared 16% (w/v) 1-ethyl-3(3-dimethylaminopropyl) carbodiimide (EDAC). After rinsed with the water, the membrane was placed on a support cushion in a clean miniblotter system (Immunetics, Inc., Cambridge, MA), and the residual water was removed from the slots. Then, the slots were filled with 150 μl of the diluted oligonucleotide solutions (approximately 200 pmol to 1 nmol of oligonucleotides in 150 μl of 50 mM $NaHCO_3$, pH 8.4). Subsequently, the membrane was incubated for 1 hr at room temperature, and then excess amount of oligonucleotide solution was removed from the slots by aspiration. In order to inactivate the membrane, the membrane was removed form the miniblotter using forceps, incubated in 100 mM NaOH for 10 min in a rolling bottle, and washed in 100 ml 2x SSPE/0.1% SDS for 5 min at 60°C in a plastic container under gentle shaking. Before applying PCR products on the ~~Biodyne~~ BIODYNE® C membrane, the membrane was incubated for 5 min at room temperature in 100 ml 2x SSPE/0.1% SDS.

IN THE CLAIMS

The claims are amended as follows.

1. (Amended) A DNA fragment which has ~~one of the sequences~~ a sequence selected from the group consisting of SEQ ~~Seq.~~ ID~~.~~ NOS:1 to 4 and ~~or~~ 6 to 24.

2. (Amended) A method ~~of diagnosis and identification Mycobacterium strain~~ for identifying the species or subspecies of a mycobacterial strain comprising the steps of:

a) digesting a DNA fragment which has ~~one~~ a sequence selected from the group consisting ~~of the sequence Seq ID. NO 1 to 4 or 6 to 24~~ SEQ ID NO:1 to SEQ ID NO:24 with at least one restriction enzyme selected from the group consisting of *Hae*III, *Msp*I, *Sau*3AI, and *Bst*EII to obtain a first DNA fragment length polymorphism pattern;

b) isolating a DNA fragment from ~~microorganisms~~ the mycobacterial strain to ~~identify~~ be identified;

c) amplifying ~~said~~ rpoB region of the DNA fragment isolated in step (b), said amplification being performed by using a primer of SEQ ID NO: 15 or SEQ ID NO: 26;

d) digesting ~~said amplified~~ the DNA fragment amplified in step c) with the at least one ~~same~~ restriction enzyme employed in step a) to obtain a second DNA fragment length polymorphism pattern; and

~~e) obtaining DNA fragment length polymorphism pattern from DNA fragment in step d); and~~

~~f)~~ e) comparing the first DNA fragment length polymorphism pattern obtained in ~~from~~ step a) with the second DNA fragment length polymorphism pattern obtained in ~~from step e)~~ step d), thereby identifying the species or subspecies of a mycobacterial strain.

3. (Amended) A method of claim 2, wherein said first and second DNA fragment length polymorphism ~~from step a) and step 3) are characterized as obtaining patterns are obtained~~ by electrophoresis.

4. (Canceled)

5. (Amended) A method of claim 2, wherein said ~~Mycobacteria~~ mycobacterial strain is selected from the group consisting of *M. tuberculosis, M. avium, M. abscessus, M. ~~flavescence~~ flavescens, M. africanum, M. bovis, ~~M. chelonae~~ M. chelonae, M. celatum, M. fortuitum, ~~M. gordonae,~~ M. gordonae, ~~M. gastri,~~ M. gastri, M. haemophilum, ~~M. intraecllulare,~~ M. intracellulare, M. kansasii, M. malmoense, M. marinum, M. szulgai, M. terrae, M. scrojulaceum, M. ulcerans,* ~~or~~ and *M. xenopi.*

IN THE DRAWINGS

Corrected Figs. 6a-6b are attached.

Marked-Up Copy of Corrections

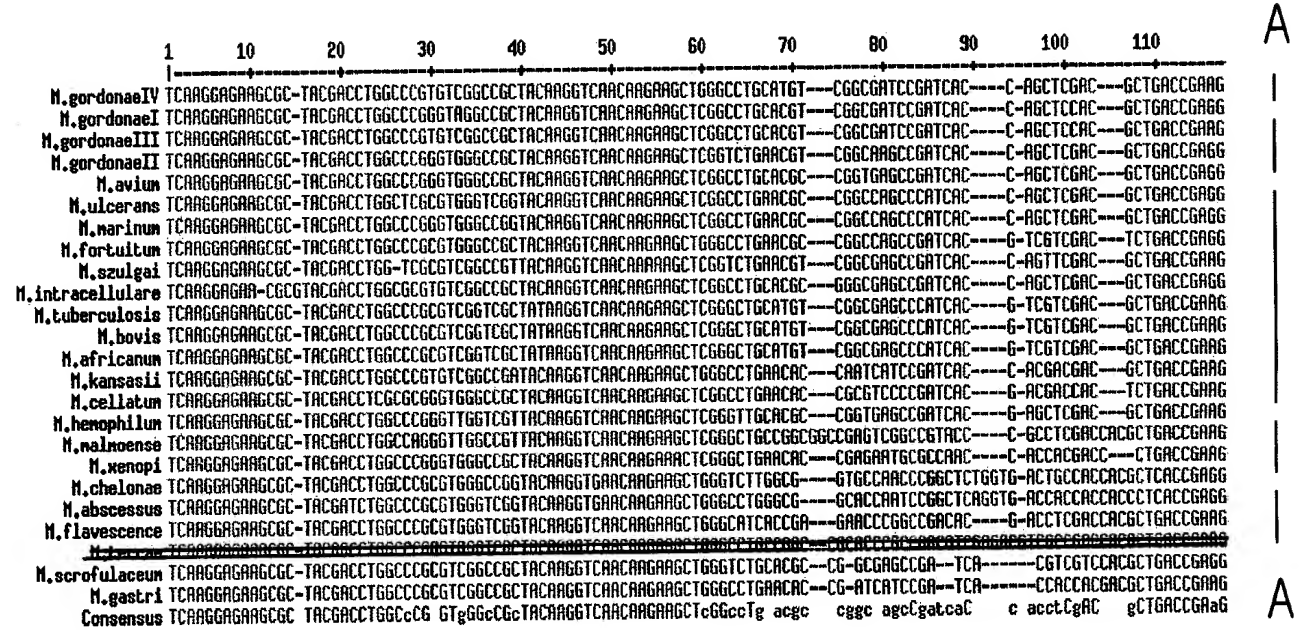

FIG. 6a

Marked-Up Copy of Corrections

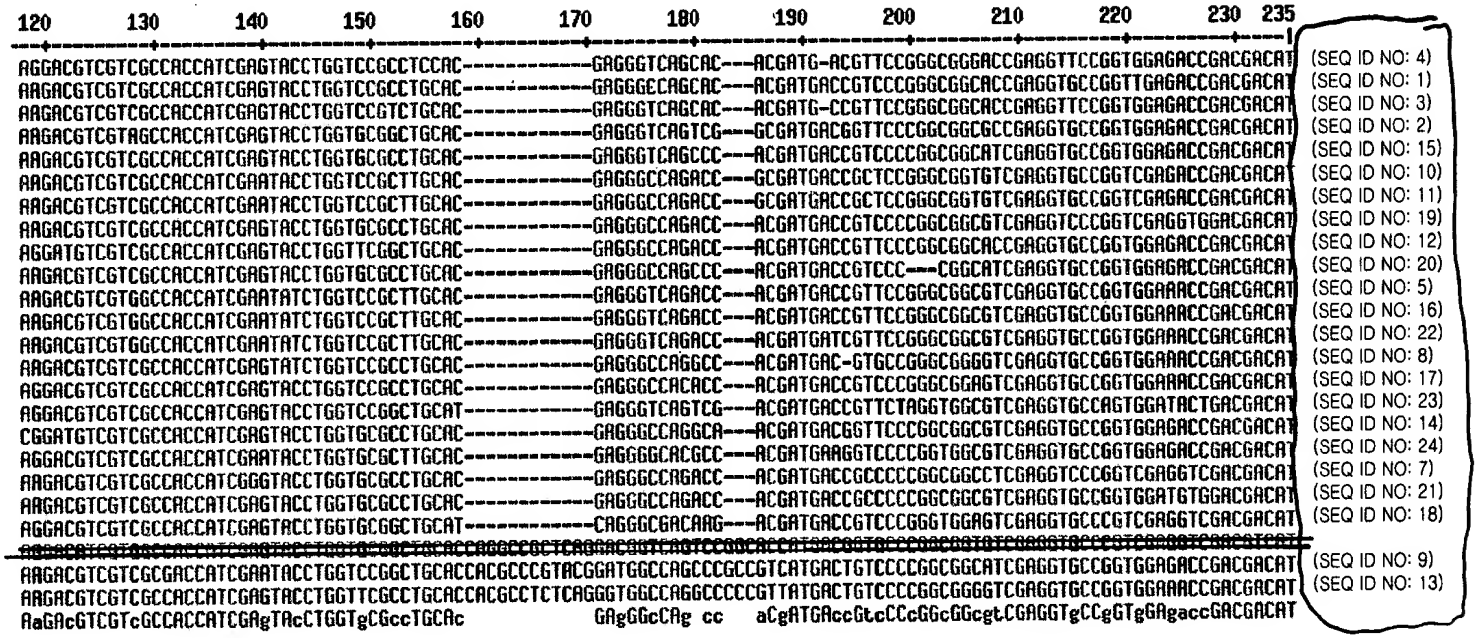

FIG. 6b